

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (currently amended) A ~~computer implemented~~ method of ~~presenting for~~ analyzing expression level information ~~as collected from first and second samples~~, said method comprising the steps of:
- obtaining a first expression level for a first expressed sequence;
 - obtaining a second expression level for said first expressed sequence;
 - obtaining information associated with said first expressed sequence, said information associated with said first expressed sequence other than said first expression level and said second expression level;
 - displaying a first axis corresponding to indicative of a value of said first expression level in said first sample;
 - displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to indicative of a value of said second expression level in said second sample;
 - and
 - for a selected expressed sequence, displaying a first mark at a first position, wherein said first position has a first coordinate is selected relative associated with to said first axis in accordance with an said first expression level of said first selected expressed sequence in said first sample and has a second coordinate relative associated with to said second axis in accordance with an said second expression level of said first selected expressed sequence in said second sample;
 - associating said first displayed mark with said obtained information associated with said first expressed sequence.
2. (currently amended) The method of claim 1 wherein said ~~selected~~ first expressed sequence comprises a gene.

3. (currently amended) The method of claim 1 wherein said selected first expressed sequence comprises a portion of a gene.

4. (currently amended) The method of claim 1 further comprising ~~the step of repeating said~~ displaying a second mark step for a second ~~a plurality of selected~~ expressed sequence sequences.

5. (currently amended) The method of claim 1 further comprising ~~the steps of: monitoring~~ obtaining said first expression level of said first expressed sequence in said a first sample and obtaining said second expression level of said first expressed sequence in said a second sample.

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6. (currently amended) The method of claim 3 5 wherein said ~~monitoring~~ obtaining said first expression level ~~step for one of said samples~~ comprises substeps of:
receiving inputting a plurality of hybridization intensities of associated with at least a pairs pair of a perfect match probe and a mismatch probe ~~probes~~, said perfect match probe ~~probes~~ being perfectly complementary to a said first expressed sequence ~~target nucleic acid~~ sequence indicative of expression of said selected gene and said mismatch ~~probes~~ probe having at least one base mismatch with said first expressed target sequence, and said plurality of hybridization intensities indicating a plurality of hybridization affinities ~~affinity~~ at least between said perfect match probe and said first expressed sequence and between said mismatch probe ~~probes~~ and ~~a sample nucleic acid~~ said first expressed sequence ~~from said one of said samples;~~
associating comparing said plurality of the hybridization intensities of for said each pair of perfect match probe and said mismatch probe; and
obtaining generating said first expression level for said first expressed sequence based on at least information associated with said plurality of hybridization intensities and ~~said one of said samples responsive to results of said comparing step.~~

7. (currently amended) The method of claim 6 further comprising ~~the step of:~~

associating comparing a difference threshold and a difference between said plurality of hybridization intensities of said perfect match and said mismatch probes at a base position to a difference threshold.

8. (currently amended) The method of claim 7 further comprising ~~the step of:~~
associating comparing a ratio threshold and a quotient of said plurality of
hybridization intensities of said perfect match probe and said mismatch probe ~~probes at a base position to a ratio threshold.~~

9. (currently amended) The method of claim 6 further comprising ~~the steps~~
of:

for each of said at least a pair of a perfect match probe and a mismatch probe,

a) counting a probe pair as a positive probe pair to increment a positive probe pair count if a perfect match probe intensity minus a mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity divided by said mismatch probe intensity exceeds a ratio threshold;

b) counting said probe pair as a negative probe pair to increment a negative probe pair count if said mismatch probe intensity minus said perfect match probe intensity exceeds said difference threshold and said mismatch probe intensity divided by said perfect match probe intensity exceeds said ratio threshold; ~~and~~

e) computing a logarithmic ratio of said perfect match probe intensity to said mismatch probe intensity;

estimating a difference of said perfect match probe intensity and said mismatch probe intensity.

10. (currently amended) The method of claim 9 further comprising ~~the steps~~
of:

~~repeating said a), b), and c) steps for each of said probe pairs, at least a pair of a perfect match probe and a mismatch probe, obtaining an average of said differences for said at least a pair of a perfect match probe and a mismatch probe;~~

~~accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that cause; and~~

~~obtaining determining an said first expression level of said selected first expressed sequence based on at least information associated with to be an said average of said differences.~~

11. (currently amended) The method of claim 1 further comprising the steps of:

receiving an user input of selection of selecting said first mark; and
in response to said user input, displaying retrieved information about associated with said first selected expressed sequence.

12. (currently amended) The method of claim 11 further comprising the steps of:

in response to said user input, displaying said retrieved information about associated with said first selected expressed sequence; said retrieved information comprising said obtained information associated with said first expressed sequence, said obtained information including an identifier for said first selected expressed sequence.

13. (currently amended) The method of claim 12 wherein said information about identifier for said first selected expressed sequence comprises a GenBank accession number.

14. (currently amended) The method of claim 12 wherein said retrieved information associated with about said first selected expressed sequence comprises a GenBank database record for said first selected expressed sequence.

15. (currently amended) The method of claim 4 5 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

16. (currently amended) The method of claim 15 wherein said particular characteristic comprises ~~presence of~~ a disease state.

17. (original) The method of claim 15 wherein said particular characteristic comprises a treatment strategy for a disease.

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18. (currently amended) The method of claim 4 15 wherein said particular characteristic is a stage of a disease.

19. (currently amended) The method of claim 1 further comprising ~~the step of:~~ displaying a third axis ~~substantially perpendicular to said first axis and to said second axis~~ in a three-dimensional display environment wherein said first position of said first mark is ~~further selected relative to~~ has a third coordinate associated with said third axis in accordance with ~~a an~~ third expression level of said first ~~selected~~ expressed sequence ~~in a third~~ sample.

20. (canceled)

21. (canceled)

22. (canceled)

23. (canceled)

24. (canceled)

25. (currently amended) A computer-readable medium including instructions ~~for program product for presenting~~ analyzing expression level information as collected from first and second samples, said product comprising:

one or more instructions for obtaining a first expression level for a first expressed sequence;

one or more instructions for obtaining a second expression level for said first expressed sequence;

one or more instructions for obtaining information associated with said first expressed sequence, said information associated with said first expressed sequence other than said first expression level and said second expression level;

one or more instructions code for displaying a first axis corresponding to indicative of a value of said first expression level in said first sample;

one or more instructions code for displaying a second axis substantially perpendicular to said first axis, said second axis corresponding to indicative of a value of said second expression level in said second sample;

one or more instructions code for, for a selected expressed sequence, displaying a first mark at a first position, wherein said first position has a first coordinate is selected relative associated with to said first axis in accordance with an said first expression level of said first selected expressed sequence in said first sample and has a second coordinate relative associated with to said second axis in accordance with an said second expression level of said first selected expressed sequence in said second sample; and

one or more instructions for associating said first displayed mark with said obtained information associated with said first expressed sequence

~~a computer-readable storage medium for storing the codes.~~

26. (currently amended) The computer-readable medium product of claim 25 wherein said selected first expressed sequence comprises a gene.

27. (currently amended) The computer-readable medium product of claim 25 wherein said ~~selected~~ first expressed sequence comprises a portion of a gene.

28. (currently amended) The computer-readable medium product of claim 25 further comprising ~~code~~ one or more instructions for ~~repeatedly applying said~~ displaying a second mark code for a second ~~a plurality of selected~~ expressed sequence sequences.

29. (currently amended) The computer-readable medium product of claim 25 further comprising: ~~code~~ one or more instructions for monitoring obtaining said first expression level of said first expressed sequence in said a first sample and obtaining said second expression level of said first expressed sequence in said a second sample.

30. (currently amended) The computer-readable medium product of claim 27 wherein said monitoring obtaining said first expression level ~~step for one of said samples~~ comprises:

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one or more instructions code for receiving inputting a plurality of hybridization intensities of associated with at least a pair pairs of a perfect match probe and a mismatch probe probes, said perfect match probe probes being perfectly complementary to a said first expressed sequence target nucleic acid sequence indicative of expression of said selected gene and said mismatch probe probes having at least one base mismatch with said first expressed target sequence, and said plurality of hybridization intensities indicating a plurality of hybridization affinity affinities at least between said perfect match probe and said first expressed sequence and between said mismatch probe probes and a sample nucleic acid said first expressed sequence from said ~~one of said samples~~;

one or more instructions for associating comparing said plurality of the hybridization intensities of for said each pair of perfect match probe and said mismatch probe; and

one or more instructions for obtaining generating said first expression level for said first expressed sequence based on at least information associated with said plurality of

hybridization intensities and ~~said one of said samples responsive to results of said comparing~~
step.

31. (currently amended) The computer-readable medium ~~product~~ of claim 30
further comprising:

one or more instructions ~~code~~ for associating ~~comparing~~ a difference threshold
and a difference between said plurality of hybridization intensities of said perfect match and said
mismatch probes at a base position to a difference threshold.

32. (currently amended) The computer-readable medium ~~product~~ of claim 31
further comprising:

one or more instructions ~~code~~ for associating ~~comparing~~ a ratio threshold and a
quotient of said plurality of hybridization intensities of said perfect match probe and said
mismatch probe probes at a base position to a ratio threshold.

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33. (currently amended) The computer-readable medium ~~product~~ of claim 30
further comprising:

for each of said at least a pair of a perfect match probe and a mismatch probe,

a) one or more instructions ~~code~~ for counting a probe pair as a positive
probe pair to increment a positive probe pair count if a perfect match probe intensity minus a
mismatch probe intensity exceeds a difference threshold and said perfect match probe intensity
divided by said mismatch probe intensity exceeds a ratio threshold;

b) one or more instructions ~~code~~ for counting said probe pair as a negative
probe pair to increment a negative probe pair count if said mismatch probe intensity minus said
perfect match probe intensity exceeds said difference threshold and said mismatch probe
intensity divided by said perfect match probe intensity exceeds said ratio threshold; and

e) one or more instructions ~~code~~ for computing a logarithmic ratio of said
perfect match probe intensity to said mismatch probe intensity;

one or more instructions for estimating a difference of said perfect match probe intensity and said mismatch probe intensity.

34. (currently amended) The computer-readable medium product of claim 33 further comprising:

one or more instructions, code for repeating said a), b), and c) codes for each of said probe pairs at least a pair of a perfect match probe and a mismatch probe, for obtaining an average of said differences for said at least a pair of a perfect match probe and a mismatch probe;

accumulating a sum of differences of said perfect match and mismatch probe intensities for probe pairs that cause; and

one or more instructions code for obtaining determining an said first expression level of said selected first expressed sequence based on at least information associated with to be an said average of said differences.

35. (currently amended) The computer-readable medium product of claim 25 further comprising:

one or more instructions code for receiving an user input of selection of selecting said first mark; and

one or more instructions code for, in response to said user input, displaying retrieved information about associated with said first selected expressed sequence.

36. (currently amended) The computer-readable medium product of claim 35 further comprising:

one or more instructions code for, in response to said user input, displaying said retrieved information about associated with said first selected expressed sequence; said retrieved information comprising said obtained information associated with said first expressed sequence, said obtained information including an identifier for said first expressed sequence.

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37. (currently amended) The computer-readable medium product of claim 36 wherein said ~~information about~~ identifier for said first ~~elected~~ expressed sequence comprises a GenBank accession number.

38. (currently amended) The computer-readable medium product of claim 36 wherein said retrieved information associated with ~~about~~ said first ~~selected~~ expressed sequence comprises a GenBank database record for said first ~~selected~~ expressed sequence.

39. (currently amended) The computer-readable medium product of claim 29 wherein said first sample and said second sample are collected from tissue samples differing in a particular characteristic.

40. (currently amended) The computer-readable medium product of claim 39 wherein said particular characteristic comprises ~~presence of~~ a disease state.

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C004 41. (currently amended) The computer-readable medium product of claim 39 wherein said particular characteristic comprises a treatment strategy for a disease.

42. (currently amended) The computer-readable medium product of claim 25 wherein said particular characteristic is a stage of a disease.

43. (currently amended) The computer-readable medium product of claim 25 further comprising ~~the step of:~~
one or more instructions for displaying a third axis substantially perpendicular to
~~said first axis and to said second axis~~ in a three-dimensional display environment wherein said
first position of said first mark is further selected relative to has a third coordinate associate with
said third axis in accordance with ~~a~~ an third expression level of said first ~~selected~~ expressed
sequence ~~in a third sample~~.

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44. (canceled)

45. (canceled)

46. (canceled)

47. (canceled)

48. (canceled)

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